Docket No.: 01017/42148

REMARKS

I.   The Rejection under 35 U.S.C. § 101 Should be Withdrawn

The Examiner rejected claims 2-3 and 7-18 under 35 U.S.C. § 101 asserting that the claims are directed to non-statutory subject matter. Claim 2 is amended to recite "isolated nucleic acid," and claims 7-9 and 11 are amended to recite "recombinant vectors." The host cells recited in claims 13-14 comprise the recombinant vector of claims 7-9 and 11. These amendments indicate that the claimed products are touched by the hand of man and therefore are statutory subject matter. Claims 3, 9, 10, 12, 16 and 18 are cancelled without prejudice. Therefore, the rejection of claims 2, 7, 8, 11, 13, 14 and 17 under 35 U.S.C. § 101 should be withdrawn.

II.   The Rejection under 35 U.S.C § 112, First Paragraph Should be Withdrawn

The Examiner rejected claims 13-18 under 35 U.S.C. § 112, first paragraph for allegedly failing to comply with the written description requirement. In particular, the Examiner asserted that the claims encompass *in vivo* cells of any transgenic non-human multicellular organism and the specification does not provide an adequate written description of transgenic animals. The terms "host cells" and "transgenic animals" are adequately described in the specification. One of skill in the art understands that the term "host cell" refers to cells used in molecular biology techniques such as DNA cloning, to receive, maintain, and allow the reproduction of recombinant DNA vectors and expression of recombinant proteins, to name a few. The specification provides many species encompassed by the genus of "host cells" (see, *e.g.* pages 27-29 of the specification). In addition, the specification describes the use of non-human mammals encoding the TP2 gene. (See, *e.g.* page 12, lines 15-25).

The Examiner also rejected claims 13-18 under 35 U.S.C. § 112, first paragraph for allegedly not being enabled by the specification. In particular, the Examiner asserted that the specification does not enable transgenic animal cells *in vivo*. The process for preparing transgenic non-human mammals are well known in the art. Further, the specification refers to the methods described in U.S. Patent No. 5,489,743 and PCT Patent Application No. WO 94/28122. (See page 12, lines 21-25). Thus, claims 12-18 are enabled by the teachings in the specification.

5

In view of the foregoing amendment and remarks, claims 13, 14, and 17 are adequately described and enabled by the specification. Therefore, the rejection under 35 U.S.C. § 112, first paragraph should be withdrawn.

III. The Rejection Under 35 U.S.C. § 112, Second paragraph Should be Withdrawn

Claims 29 and 30 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite for failing to particular point out and distinctly claim the subject matter of the invention. Claims 29 and 30 are amended to recite "the amino acid position at 868 of SEQ ID NO: 20" rather than SEQ ID NO: 19. As SEQ ID NO: 19 is a polynucleotide sequence that comprises nucleotides rather than amino acids, the reference to SEQ ID NO: 19 was a typographical error. In view of the foregoing amendment, the rejection of claims 29 and 30 under 35 U.S.C. § 112, second paragraph should be withdrawn.

IV. The Rejection Under 35 U.S.C. § 102 Should be Withdrawn

Claims 1, 4, 6, 7, 12, 13, 16, 18-20 and 26-27 were rejected under 35 U.S.C. § 102(e) as allegedly being anticipated by Cech *et al*, U.S. Patent No. 6,6,261,836 (denoted herein as Cech '836). The Examiner stated the polynucleotide sequence of SEQ ID NO: 224 of Cech '836 is identical to nucleotides 13-3798 of SEQ ID NO: 19 of the present invention. Amended claims 1, 26 and 27 are directed to the nucleotide sequence of SEQ ID NO: 13, SEQ ID NO: 19, and nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 14 or SEQ ID NO: 20. The polynucleotide sequence of SEQ ID NO: 224 in Cech '836 is not 100% identical to the claim-recited polynucleotide sequences of SEQ ID NO: 13 and SEQ ID NO: 19. (See attached alignments in Exhibit A). In addition, the amino acid sequence of SEQ ID NO: 225, which is encoded by the polynucleotide sequence of SEQ ID NO: 223 is not 100% identical to the full length amino acid sequence of SEQ ID NO: 14 or SEQ ID NO: 20. (See attached alignments in Exhibit B). Claims 4, 6, 12, 16 and 18-20 are canceled without prejudice. Therefore, the amended claims are not anticipated by the polynucleotide sequence of SEQ ID NO: 224 in Cech '836 and the rejection of claims 1, 13, 26 and 27 under 35 U.S.C. § 102(e) should be withdrawn.

The Examiner also rejected claims 28-30 under 35 U.S.C. §102(e) as allegedly being anticipated by Cech *et al*, U.S. Patent No. 6,475,789 (denoted herein as Cech '789). Claim 28 is directed to variant polypeptides of SEQ ID NO: 13 or SEQ ID NO: 19, and claims 29 and 30 are directed to specific variants and mutants of SEQ ID NO: 19. Cech '789 generally provides variants of human telomerase catalytic subunit and a mutant plasmid in which Asp869 is

6

Docket No.: 01017/42148

substituted with an alanine. However, Cech '789 does not teach any sequences in which Asp868 is changed to the amino acid alanine. The Examiner points to column 198, line 14-15 of Cech '789 to support her statements, but that portion of Cech '789 provides SEQ ID NOS: 51, 52 and 53 which are 55, 34 and 35 amino acids in length, respectively. Therefore, amended claims 28-30 are directed to variant and mutant nucleic acids in which the codon for Asp838, is changed to the amino acid alanine and are not anticipated by Cech '769. Thus, the rejection of claims 28-30 under 35 U.S.C. § 102(e) should be withdrawn.
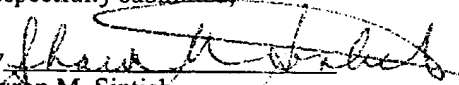
On page 7 of the Action, the Examiner stated that SEQ ID NO: 13 contains the same additional 12 nucleotides at the 5' end as SEQ ID NO: 19 and these 12 nucleotides are not identical to SEQ ID NO: 224 in Cech '836. However, this statement is incorrect; nucleotides 12-2848 SEQ ID NO: 13 are identical to nucleotides 1-2837 of SEQ ID NO: 224 of Cech '836.

CONCLUSION

In view of the foregoing amendment and remarks, Applicants believe claims 1, 2, 5, 7, 8, 11, 13, 14, 17, 26-30 and 33 are in condition for allowance and early notice thereof is requested.

Respectfully submitted,

Dated: August 21, 2006

By Sharon M. Sintich
Registration No.: 48,484
MARSHALL GERSTEIN & BORUN
233 S. Wacker Drive, Suite 6300
Sears Tower
Chicago, Illinois 60606-6357
(312) 474-6300
Attorneys for Applicant

7

Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: |1   Mismatch: |-2   gap open: |5   gap extension: |2
x_dropoff: |50   expect: |10.000| wordsize: |11   Filter ⎕   View option |Standard   ⎥|
Masking character option |X for protein, n for nucleotide ⎥| Masking color option |Black ⎥|
⎕ Show CDS translation   Align|

Sequence 1: lcl|1_seq_1   SEQ ID NO:3 (08/951,773)
Length = 2848 (1 .. 2848)

Sequence 2: lcl|2_seq_2   SEQ ID NO:224 (Cech '789)
Length = 4015 (1 .. 4015)
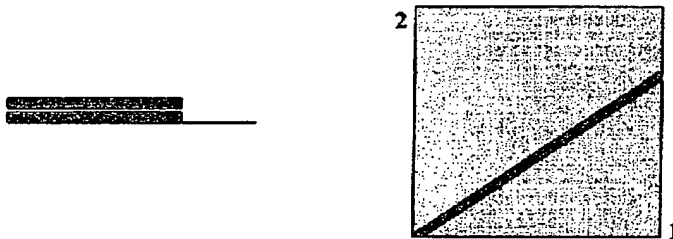
NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
Score = 5455 bits (2837),  Expect = 0.0
Identities = 2837/2837 (100%),  Gaps = 0/2837 (0%)
Strand=Plus/Plus

Query  12    GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC  71
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC  60

Query  72    GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT  120

Query  132   GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG  180
```

Blast Result   Page 2 of 5

```
Query  192  GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  240

Query  252  ACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  300

Query  312  CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC  371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC  360

Query  372  GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  431
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  420

Query  432  CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG  491
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG  480

Query  492  CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT  551
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT  540

Query  552  GGCTCCCAGCTGCGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC  611
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGCTCCCAGCTGCGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC  600

Query  612  TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC  671
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC  660

Query  672  CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG  731
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG  720

Query  732  GAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC  791
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  GAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC  780

Query  792  TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC  851
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC  840

Query  852  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC  911
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841  GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC  900

Query  912  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA  971
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901  CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA  960

Query  972  GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC  1031
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961  GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC  1020

Query  1032 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1091
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

```
Query  1092  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA  1151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA  1140

Query  1152  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT  1211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT  1200

Query  1212  GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260

Query  1272  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC  1331
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC  1320

Query  1332  AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA  1391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321  AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA  1380

Query  1392  CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA  1451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381  CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA  1440

Query  1452  CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCA  1511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441  CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCA  1500

Query  1512  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Query  1572  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG  1631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG  1620

Query  1632  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1680

Query  1692  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA  1751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA  1740

Query  1752  TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1741  TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG  1800

Query  1812  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860

Query  1872  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG  1931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG  1920

Query  1932  CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1921  CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
```

```
Query  1992  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT  2051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1981  CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT  2040

Query  2052  CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG  2111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2041  CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG  2100

Query  2112  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC  2171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2101  CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC  2160

Query  2172  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA  2231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2161  GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA  2220

Query  2232  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG  2291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2221  GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG  2280

Query  2292  TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA  2351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2281  TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA  2340

Query  2352  CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2341  CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA  2400

Query  2412  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG  2471
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2401  GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG  2460

Query  2472  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG  2531
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2461  CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG  2520

Query  2532  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG  2591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2521  CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG  2580

Query  2592  CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT  2651
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2581  CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT  2640

Query  2652  GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC  2711
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2641  GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC  2700

Query  2712  CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA  2771
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2701  CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA  2760

Query  2772  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT  2831
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2761  GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT  2820

Query  2832  GCCGGCCCACGGCCTAT  2848
             |||||||||||||||||
Sbjct  2821  GCCGGCCCACGGCCTAT  2837
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

Blast Result   Page 5 of 5

```
CPU time:      0.02 user secs.       0.01 sys. secs       0.03 total secs.

Lambda      K       H
    1.33    0.621     1.12

Gapped
Lambda      K       H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 996
Number of extensions: 29
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 2848
Length of database: 17,735,149,364
Length adjustment: 27
Effective length of query: 2821
Effective length of database: 17,735,149,337
Effective search space: 50030856279677
Effective search space used: 50030856279677
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 15 (29.5 bits)
S2: 22 (43.0 bits)
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure
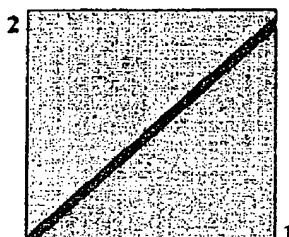
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

Match: |1   Mismatch: |-2   gap open: |5   gap extension: |2

x_dropoff: |50   expect: |10.000' wordsize: |11   Filter ⌐ View option |Standard   ⬆|

Masking character option |X for protein, n for nucleotide ⬇| Masking color option |Black ⬇|

⌐ Show CDS translation |Align|

Sequence 1: lcl|1_seq_1   SEQ ID NO: 19 (08|951,773)
Length = 3798 (1 .. 3798)

Sequence 2: lcl|2_seq_2   SEQ ID NO: 224 (Each '789)
Length = 4015 (1 .. 4015)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 7274 bits (3783),  Expect = 0.0
 Identities = 3785/3786 (99%), Gaps = 0/3786 (0%)
 Strand=Plus/Plus

Query  13    GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC   72
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC   60

Query  73    GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT   132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT   120

Query  133   GCCGCTGGCCACGTTCGTGCGGCGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG   192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCCGCTGGCCACGTTCGTGCGGCGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG   180
```

· Blast Result

```
Query  193   GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  252
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  240

Query  253   ACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  312
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ACGGCCGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGC  300

Query  313   CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC  372
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC  360

Query  373   GCTGCTGGACGGGGCCCGCGGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  432
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GCTGCTGGACGGGGCCCGCGGGGGGCCCCCCCGAGGCCTTCACCACCAGCGTGCGCAGCTA  420

Query  433   CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG  492
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG  480

Query  493   CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT  552
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT  540

Query  553   GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC  612
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCAC  600

Query  613   TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC  672
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC  660

Query  673   CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG  732
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAG  720

Query  733   GAGGCGCGGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC  792
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   GAGGCGCGGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC  780

Query  793   TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC  852
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   TGCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGAC  840

Query  853   GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC  912
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC  900

Query  913   CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA  972
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCA  960

Query  973   GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC  1032
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961   GCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC  1020

Query  1033  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1092
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021  CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG  1080
```

```
Query  1093  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA  1152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA  1140

Query  1153  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT  1212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT  1200

Query  1213  GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201  GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA  1260

Query  1273  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC  1332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261  GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC  1320

Query  1333  AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA  1392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321  AGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGA  1380

Query  1393  CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA  1452
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381  CACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA  1440

Query  1453  CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCA  1512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441  CGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCA  1500

Query  1513  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501  CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA  1560

Query  1573  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG  1632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561  GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG  1620

Query  1633  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1621  GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC  1680

Query  1693  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA  1752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1681  CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA  1740

Query  1753  TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTGTCTGGAG  1812
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1741  TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTGTCTGGAG  1800

Query  1813  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1801  CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC  1860

Query  1873  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG  1932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1861  GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG  1920

Query  1933  CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1921  CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC  1980
```

```
Query   1993   CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT   2052
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1981   CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT   2040

Query   2053   CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG   2112
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2041   CAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG   2100

Query   2113   CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC   2172
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2101   CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCC   2160

Query   2173   GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA   2232
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2161   GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA   2220

Query   2233   GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG   2292
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2221   GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG   2280

Query   2293   TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA   2352
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2281   TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA   2340

Query   2353   CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA   2412
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2341   CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA   2400

Query   2413   GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG   2472
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2401   GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG   2460

Query   2473   CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG   2532
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2461   CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG   2520

Query   2533   CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG   2592
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2521   CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG   2580

Query   2593   CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT   2652
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2581   CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT   2640

Query   2653   GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC   2712
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2641   GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC   2700

Query   2713   CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA   2772
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2701   CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA   2760

Query   2773   GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT   2832
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2761   GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT   2820

Query   2833   GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT   2892
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   2821   GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT   2880
```

Blast Result   Page 5 of 6

```
Query  2893  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG  2952
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2881  GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG  2940

Query  2953  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG  3012
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2941  CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG  3000

Query  3013  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA  3072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3001  TCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA  3060

Query  3073  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA  3132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3061  CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA  3120

Query  3133  TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3121  TCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCT  3180

Query  3193  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGGCCAAGGGCGCCGC  3252
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3181  CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGGCCAAGGGCGCCGC  3240

Query  3253  CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3241  CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT  3300

Query  3313  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA  3372
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3301  GACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCA  3360

Query  3373  GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC  3432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3361  GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC  3420

Query  3433  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA  3492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3421  ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGA  3480

Query  3493  GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC  3552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3481  GAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCC  3540

Query  3553  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG  3612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3541  CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG  3600

Query  3613  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3601  CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT  3660

Query  3673  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  3732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3661  GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA  3720

Query  3733  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3792
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3721  GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC  3780
```

Blast Result   Page 6 of 6


```
Query  3793  CCTGAT  3798
             || |||
Sbjct  3781  CCAGAT  3786
```


CPU time: 0.02 user secs.   0.00 sys. secs   0.02 total secs.

```
Lambda     K       H
  1.33     0.621     1.12

Gapped
Lambda     K       H
  1.33     0.621     1.12
```


```
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 1326
Number of extensions: 40
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 3798
Length of database: 17,737,237,516
Length adjustment: 27
Effective length of query: 3771
Effective length of database: 17,737,237,489
Effective search space: 66887122571019
Effective search space used: 66887122571019
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 15 (29.5 bits)
S2: 22 (43.0 bits)
```


http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/19/2006

Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

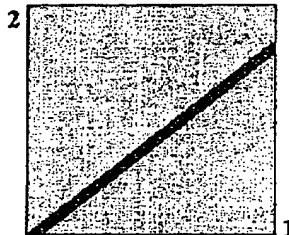## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ▾ gap open: 11   gap extension: 1
x_dropoff: 50   expect: 10.000 wordsize: 3   Filter ☐   View option Standard ▾
Masking character option X for protein, n for nucleotide ▾   Masking color option Black ▾
☐ Show CDS translation   Align

Sequence 1: lcl|1_seq_1   *SEQ ID NO:14 (08AS1,773)*
Length = 949 (1 .. 949)

Sequence 2: lcl|2_seq_2   *SEQ ID NO:225 (Coch '789)*
Length = 1132 (1 .. 1132)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 1892 bits (4900),  Expect = 0.0
 Identities = 927/927 (100%),  Positives = 927/927 (100%),  Gaps = 0/927 (0%)

Query   23   MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW   82
             MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW
Sbjct   1    MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW   60

Query   83   DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR   142
             DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR
Sbjct   61   DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR   120

Query   143  SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA   202
             SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA
Sbjct   121  SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA   180

Query   203  ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR   262
             ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR
Sbjct   181  ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR   240
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

```
Query   263  GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG  322
             GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
Sbjct   241  GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG  300

Query   323  RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL  382
             RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
Sbjct   301  RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL  360

Query   383  VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT  442
             VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT
Sbjct   361  VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT  420

Query   443  PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS  502
             PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
Sbjct   421  PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS  480

Query   503  RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI  562
             RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
Sbjct   481  RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI  540

Query   563  LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFPYRKSVWSKLQSIGIRQHLKRVQLRE  622
             LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFPYRKSVWSKLQSIGIRQHLKRVQLRE
Sbjct   541  LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFPYRKSVWSKLQSIGIRQHLKRVQLRE  600

Query   623  LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA  682
             LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
Sbjct   601  LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA  660

Query   683  LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI  742
             LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI
Sbjct   661  LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI  720

Query   743  PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAPKSHVSTLTDLQPYMRQFVAHL  802
             PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAPKSHVSTLTDLQPYMRQFVAHL
Sbjct   721  PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAPKSHVSTLTDLQPYMRQFVAHL  780

Query   803  QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL  862
             QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
Sbjct   781  QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL  840

Query   863  LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL  922
             LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL
Sbjct   841  LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL  900

Query   923  RKTVVNFPVEDEALGGTAFVQMPAHGL  949
             RKTVVNFPVEDEALGGTAFVQMPAHGL
Sbjct   901  RKTVVNFPVEDEALGGTAFVQMPAHGL  927
```

CPU time: 0.04 user secs.   0.01 sys. secs   0.05 total secs.

```
Lambda      K      H
  0.324   0.136    0.438

Gapped
Lambda      K      H
  0.267   0.0410   0.140
```

Blast Result   Page 3 of 3

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 9263
Number of extensions: 5430
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 1
Length of query: 949
Length of database: 1,308,253,377
Length adjustment: 144
Effective length of query: 805
Effective length of database: 1,308,253,233
Effective search space: 1053143852565
Effective search space used: 1053143852565
Neighboring words threshold: 9
X1: 15 ( 7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 84 (37.0 bits)
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix [BLOSUM62 ▾] gap open: [11]   gap extension: [1]
x_dropoff: [50] expect: [10.000] wordsize: [3]   Filter ⌐ View option [Standard ▾]
Masking character option [X for protein, n for nucleotide ▾]   Masking color option [Black ▾]
⌐ Show CDS translation [Align]

Sequence 1: lcl|1_seq_1
Length = 1154 (1 .. 1154)   *SEQ ID NO:20 (08/951,773)*

Sequence 2: lcl|2_seq_2
Length = 1132 (1 .. 1132)   *SEQ ID NO:225 (Cech '789)*
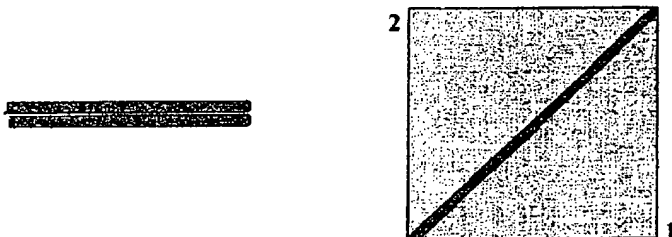
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 2300 bits (5961),  Expect = 0.0
 Identities = 1132/1132 (100%), Positives = 1132/1132 (100%), Gaps = 0/1132 (0%)

Query   23   MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW   82
             MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW
Sbjct   1    MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW   60

Query   83   DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR   142
             DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR
Sbjct   61   DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR   120

Query   143  SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA   202
             SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA
Sbjct   121  SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA   180

Query   203  ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR   262
             ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR
Sbjct   181  ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR   240
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

Blast Result   Page 2 of 3

```
Query   263  GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG  322
             GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
Sbjct   241  GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG  300

Query   323  RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL  382
             RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
Sbjct   301  RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL  360

Query   383  VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT  442
             VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLBLLGNHAQCPYGVLLKTHCPLRAAVT
Sbjct   361  VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLBLLGNHAQCPYGVLLKTHCPLRAAVT  420

Query   443  PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS  502
             PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
Sbjct   421  PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS  480

Query   503  RHNERRPLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI  562
             RHNERRPLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
Sbjct   481  RHNERRPLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI  540

Query   563  LAKPLHWLMSVYVVELLRSFFYVTETTPQKNRLPFYRKSVWSKLQSIGIRQHLKRVQLRB  622
             LAKPLHWLMSVYVVELLRSFFYVTETTPQKNRLPFYRKSVWSKLQSIGIRQHLKRVQLRB
Sbjct   541  LAKPLHWLMSVYVVELLRSFFYVTETTPQKNRLPFYRKSVWSKLQSIGIRQHLKRVQLRB  600

Query   623  LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA  682
             LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
Sbjct   601  LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA  660

Query   683  LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI  742
             LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI
Sbjct   661  LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI  720

Query   743  PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL  802
             PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
Sbjct   721  PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL  780

Query   803  QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL  862
             QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
Sbjct   781  QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL  840

Query   863  LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL  922
             LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL
Sbjct   841  LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL  900

Query   923  RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF  982
             RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
Sbjct   901  RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF  960

Query   983  NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP  1042
             NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP
Sbjct   961  NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP  1020

Query   1043 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL  1102
             FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL
Sbjct   1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL  1080

Query   1103 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD  1154
             KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD
Sbjct   1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD  1132
```

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006

CPU time: 0.04 user secs.   0.01 sys. secs   0.05 total secs.

Lambda   K   H
   0.324   0.138   0.434

Gapped
Lambda   K   H
   0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 10,897
Number of extensions: 6421
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1154
Length of database: 1,308,253,377
Length adjustment: 145
Effective length of query: 1009
Effective length of database: 1,308,253,232
Effective search space: 1320027511088
Effective search space used: 1320027511088
Neighboring words threshold: 9
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 84 (37.0 bits)

http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0   7/18/2006